



81408-4400.ST25.txt

SEQUENCE LISTING

<110> ProChon Biotech, Ltd.
MorphoSys AG
Yayon, Avner
Thomassen-Wolf, Elisabeth
Rom, Eran
Borges, Eric

<120> ANTIBODIES THAT BLOCK RECEPTOR PROTEIN TYROSINE KINASE ACTIVATION

<130> 81408-4400

<140> US 10/734,661
<141> 2003-12-15

<150> US 60/299,187
<151> 2001-06-20

<150> PCT/IL02/00494
<151> 2002-06-20

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<400> 27

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<400> 29

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 <302> Fully synthetic human combinatorial antibody libraries (HuCAL)
 based on modular consensus frameworks and CDRs randomized with
 trinucleotides.
 <303> J Mol Biol
 <304> 296
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 <306> 57-86
 <307> 2000-02-11
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based on modular consensus frameworks and CDRs randomized with

trinucleotides.
<303> j mol biol
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<220>
<223> polynucleotide sequence of a VL domain

<220>
<221> misc_feature
<222> (256)..(258)
<223> NNN=ACT OR GTT

<400> 56
gatatcgtgc tgaccagag cccggcgacc ctgaggctgt ctccggcgaa acgtgcgacc 60
ctgagctgca gagcggccca gagcgtgagc agcagctatc tggcgtggta ccagcagaaa 120
ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tggggtcccg 180
gcccgtttta gcggctctgg atccggcactg gattttaccc tgaccattag cagcctggaa 240
cctgaagact ttgcgnnta ttattgccag acctttggcc agggtacgaa agttgaaatt 300
aaacgtacg 309

<210> 57
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VL domain

<400> 57
gatatcgtgc tgaccagag cccggcgacc ctgaggctgt ctccggcgaa acgtgcgacc 60
ctgagctgca gagcggccca gagcgtgagc agcagctatc tggcgtggta ccagcagaaa 120
ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tggggtcccg 180
gcccgtttta gcggctctgg atccggcactg gattttaccc tgaccattag cagcctggaa 240
cctgaagact ttgcgactta ttattgccag cagatgtcta attatcctga tacctttggc 300
cagggtacga aagttgaaat taaacgtacg 330

<210> 58
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VL domain

<400> 58
gatatcgtgc tgaccagag cccggcgacc ctgaggctgt ctccggcgaa acgtgcgacc 60
ctgagctgca gagcggccca gagcgtgagc agcagctatc tggcgtggta ccagcagaaa 120
ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tggggtcccg 180
gcccgtttta gcggctctgg atccggcactg gattttaccc tgaccattag cagcctggaa 240
cctgaagact ttgcgactta ttattgccag cagactaata atgctctgt tacctttggc 300
cagggtacga aagttgaaat taaacgtacg 330

<210> 59
<211> 324
<212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VL domain

<400> 59

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attaactgca	gaaggagcca	gagcgtgctg	tatagcagca	acaacaaaaaa	ctatctggcg	120
tggtaccagc	agaaaccagg	tcagccggcg	aaactattaa	tttattggc	atccacccgt	180
gaaagcgggg	tcccgatcg	tttttagccgc	tctggatccg	gcactgattt	taccctgacc	240
atttcgtccc	tgcaagctga	agacgtggcg	gtgtattatt	gccagacctt	tggccagggt	300
acgaaagtt	aaattaaacg	tacg				324

<210> 60

<211> 345

<212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VL domain

<400> 60

gatatcgta	tgacccagag	cccggatagc	ctggcggtga	gcctggcg	acgtgcgacc	60
attaactgca	gaaggagcca	gagcgtgctg	tatagcagca	acaacaaaaaa	ctatctggcg	120
tggtaccagc	agaaaccagg	tcagccggcg	aaactattaa	tttattggc	atccacccgt	180
gaaagcgggg	tcccgatcg	tttttagccgc	tctggatccg	gcactgattt	taccctgacc	240
atttcgtccc	tgcaagctga	agacgtggcg	gtgtattatt	gccagcagta	tgattctatt	300
ccttataacct	ttggccagggt	tacgaaagtt	gaaattaaac	gtacg		345

<210> 61

<211> 315

<212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VL domain

<400> 61

gatatcgcac	tgacccagcc	agcttcagtg	agcggctcac	caggtcagag	cattaccatc	60
tctgtacgg	gtactagcag	cgatgtggc	ggctataact	atgtgagctg	gtaccagcag	120
catccccggg	aggcgccgaa	actgatgatt	tatgatgtga	gcaaccgtcc	ctcaggcgtg	180
agcaaccgtt	ttagcggatc	caaagcggc	aacaccgcga	gcctgaccat	tagcggcgtg	240
caagcggaaag	acgaagcggaa	ttattattgc	caggacgtgt	ttggcggcgg	cacgaagtta	300
accgttcttg	gccag					315

<210> 62

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VL domain

<400> 62

gatatcgcac	tgacccagcc	agcttcagtg	agcggctcac	caggtcagag	cattaccatc	60
tctgtacgg	gtactagcag	cgatgtggc	ggctataact	atgtgagctg	gtaccagcag	120
catccccggg	aggcgccgaa	actgatgatt	tatgatgtga	gcaaccgtcc	ctcaggcgtg	180
agcaaccgtt	ttagcggatc	caaagcggc	aacaccgcga	gcctgaccat	tagcggcgtg	240

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caagcggaaag acgaagcgg a ttattattgc cagagctatg acatgtataa ttatattgtg	300
tttggccggc gcacgaagtt aaccgttctt ggccag	336
<210> 63	
<211> 330	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> polynucleotide sequence of a VL domain	
<400> 63	
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tcgtgtacgg gtacttagcag cgatgtggc ggctataact atgtgagctg gtaccagcag	120
catcccggga aggccccgaa actgatgatt tatgatgtga gcaaccgtcc ctcaggcgtg	180
agcaaccgtt ttagcggatc caaaagcggc aacaccgcga gcctgaccat tagcggcctg	240
caagcggaaag acgaagcgg a ttattattgc cagtcctatc atttttatga ggtgtttggc	300
ggccggcactga agttaaccgt tcttggccag	330
<210> 64	
<211> 336	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> polynucleotide sequence of a VL domain	
<400> 64	
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tcgtgtacgg gtacttagcag cgatgtggc ggctataact atgtgagctg gtaccagcag	120
catcccggga aggccccgaa actgatgatt tatgatgtga gcaaccgtcc ctcaggcgtg	180
agcaaccgtt ttagcggatc caaaagcggc aacaccgcga gcctgaccat tagcggcctg	240
caagcggaaag acgaagcgg a ttattattgc cagagctatg acaataattc tgatgttgtg	300
tttggccggc gcacgaagtt aaccgttctt ggccag	336
<210> 65	
<211> 306	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> polynucleotide sequence of a VL domain	
<400> 65	
gatatcgaaac tgacctcagcc gccttcagtg agcggtgcac caggtcagac cgccgcgtatc	60
tcgtgtacgg gcgtatgcgtc gggcgataaa tacgcgagct ggtaccagca gaaaccgggg	120
caggcgccag ttctgggtat ttatgatgat tctgaccgtc cctcaggcat cccggAACgc	180
tttagcggat ccaacagcgg caacaccgcg accctgacca ttagcggcac tcaggcggaa	240
gacgaagcgg attattattg ccaggacgtg tttggccggc gcacgaagtt aaccgttctt	300
ggccag	306
<210> 66	
<211> 324	
<212> DNA	
<213> Artificial Sequence	
<220>	

<223> polynucleotide sequence of a VL domain

<400> 66

gatatcgaac	tgaccaggcc	gccttcagtg	agcgttgcac	caggtcagac	cgcgcgtatc	60
tcgtgttagcg	gcgatgcgct	gggcgataaaa	tacgcgagct	ggtaccagca	gaaaccggg	120
caggcgccag	ttctgggtat	ttatgtat	tctgaccgto	cctcaggcat	cccggAACGC	180
tttagcggat	ccaacagcgg	caacaccgct	accctgacca	ttagcggcac	tcagggcggaa	240
gacgaagcgg	attattattt	ccagagctat	gactattta	agcttgtt	tggcggcggc	300
acgaagttaa	ccgttcttgg	ccag				324

<210> 67

<211> 327

<212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VL domain

<400> 67

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tcgtgttagcg	gcgatgcgct	gggcgataaaa	tacgcgagct	ggtaccagca	gaaaccggg	120
caggcgccag	ttctgggtat	ttatgtat	tctgaccgto	cctcaggcat	cccggAACGC	180
tttagcggat	ccaacagcgg	caacaccgct	accctgacca	ttagcggcac	tcagggcggaa	240
gacgaagcgg	attattattt	ccagagctat	gactattctg	ctgattatgt	gtttggcggc	300
ggcacgaagt	taaccgttct	tggccag				327

<210> 68

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VL domain

<400> 68

gatatcgaac	tgaccaggcc	gccttcagtg	agcgttgcac	caggtcagac	cgcgcgtatc	60
tcgtgttagcg	gcgatgcgct	gggcgataaaa	tacgcgagct	ggtaccagca	gaaaccggg	120
caggcgccag	ttctgggtat	ttatgtat	tctgaccgto	cctcaggcat	cccggAACGC	180
tttagcggat	ccaacagcgg	caacaccgct	accctgacca	ttagcggcac	tcagggcggaa	240
gacgaagcgg	attattattt	ccagagctat	gactttgatt	ttgcttgtt	tggcggcggc	300
acgaagttaa	ccgttcttgg	ccag				324

<210> 69

<211> 327

<212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VL domain

<400> 69

gatatcgaac	tgaccaggcc	gccttcagtg	agcgttgcac	caggtcagac	cgcgcgtatc	60
tcgtgttagcg	gcgatgcgct	gggcgataaaa	tacgcgagct	ggtaccagca	gaaaccggg	120
caggcgccag	ttctgggtat	ttatgtat	tctgaccgto	cctcaggcat	cccggAACGC	180
tttagcggat	ccaacagcgg	caacaccgct	accctgacca	ttagcggcac	tcagggcggaa	240
gacgaagcgg	attattattt	ccagagctat	gacggtcctg	atctttgggt	gtttggcggc	300
ggcacgaagt	taaccgttct	tggccag				327

<210> 70
<211> 332
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VH domain

<220>
<221> misc_feature
<222> (1)..(3)
<223> NNN=GAA OR CAG

<400> 70
nnngtcaat tggttcagtc tggcgcgaa gtaaaaaac cgggcagcag cgtaaaagtg 60
agctgcaaag cctccggagg cacttttagc agctatgcga tttagctgggt gcgccaagcc 120
cctggcagg gtctcgagtg gatgggcggc attattccga ttttggcac ggcgaactac 180
gcccagaagt ttcagggccg ggtgaccatt accgcggatg aaagcaccag caccgcgtat 240
atggaactga gcagcctgctg tagcgaagat acggccgtgt attattgcgc gcgtgattgg 300
ggccaaggca ccctggtgac gtttagctca gc 332

<210> 71
<211> 359
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VH domain.

<400> 71
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agctgcaaag cctccggagg cacttttagc agctatgcga tttagctgggt gcgccaagcc 120
cctggcagg gtctcgagtg gatgggcggc attattccga ttttggcac ggcgaactac 180
gcccagaagt ttcagggccg ggtgaccatt accgcggatg aaagcaccag caccgcgtat 240
atggaactga gcagcctgctg tagcgaagat acggccgtgt attattgcgc gcgtgataat 300
tggtaaagc cttttctga tggtgggc caaggcaccc tggtgacggc tagctcagc 359

<210> 72
<211> 359
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VH domain

<400> 72
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agctgcaaag cctccggagg cacttttagc agctatgcga tttagctgggt gcgccaagcc 120
cctggcagg gtctcgagtg gatgggcggc attattccga ttttggcac ggcgaactac 180
gcccagaagt ttcagggccg ggtgaccatt accgcggatg aaagcaccag caccgcgtat 240
atggaactga gcagcctgctg tagcgaagat acggccgtgt attattgcgc gcgtgttaat 300
cattggactt atactttga ttattgggc caaggcaccc tggtgacggc tagctcagc 359

<210> 73
<211> 374
<212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VH domain

<400> 73

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agctgcaaag cctccggagg cacttttagc agctatgcga tttagctgggt ggcggcaagcc	120
cctggcagg gtctcgagt gatgggcggc attattccga ttttggcac ggcgaactac	180
gcccagaagt ttcatggccg ggtgaccatt accgcggatg aaagcaccag caccgcgtat	240
atgaaactga gcagcctgct tagcgaagat acggccgtgt attattgcgc gcgtgggtgt	300
ggttgggtt ctatggta ttattatctt tttagatctt gggccaagg caccctggtg	360
acggtagct cagc	374

<210> 74

<211> 332

<212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VH domain

<220>

<221> misc_feature

<222> (1)..(3)

<223> NNN=GAA OR CAG

<400> 74

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agctgcaaag cctccggata taccttacc agctattata tgcactgggt cgcggcaagcc	120
cctggcagg gtctcgagt gatgggcgtt attaaccga atagcggcgg cacgaactac	180
gcccagaagt ttcatggccg ggtgaccatg acccgtgata ccagcattag caccgcgtat	240
atgaaactga gcagcctgct tagcgaagat acggccgtgt attattgcgc gcgtgattgg	300
ggccaaggca ccctggtgac ggttagctca gc	332

<210> 75

<211> 380

<212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VH domain

<400> 75

caggtcaat tggttcagag cggcgcgaa gtaaaaaac cgggcgcgag cgtaaaagtg	60
agctgcaaag cctccggata taccttacc agctattata tgcactgggt cgcggcaagcc	120
cctggcagg gtctcgagt gatgggcgtt attaaccga atagcggcgg cacgaactac	180
gcccagaagt ttcatggccg ggtgaccatg acccgtgata ccagcattag caccgcgtat	240
atgaaactga gcagcctgct tagcgaagat acggccgtgt attattgcgc gcgtaatatg	300
gcttatacta attatcagta tgttaatatg cctcatatgtt attattgggg ccaaggcacc	360
ctggtagcgg ttagctcagc	380

<210> 76

<211> 380

<212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VH domain

<400> 76

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agctgcaaag	cctccggata	taccttacc	agctattata	tgcactgggt	ccgccaagcc	120
cctggcagg	gtctcgagt	gatgggctgg	attaaccga	atagcggcgg	cacgaactac	180
gcccagaagt	ttcagggccg	ggtgaccatg	accctgtata	ccagcattag	caccgcgtat	240
atggaactga	gcagcctg	tagcgaagat	acggccgtgt	attattgcgc	gcgttctatg	300
aattctacta	tgtattgta	tcttcgtcgt	gttcttttg	atcattgggg	ccaaggcacc	360
ctgggtacgg	ttagctcagc					380

<210> 77

<211> 356

<212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VH domain

<400> 77

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agctgcaaag	cctccggata	taccttacc	agctattata	tgcactgggt	ccgccaagcc	120
cctggcagg	gtctcgagt	gatgggctgg	attaaccga	atagcggcgg	cacgaactac	180
gcccagaagt	ttcagggccg	ggtgaccatg	accctgtata	ccagcattag	caccgcgtat	240
atggaactga	gcagcctg	tagcgaagat	acggccgtgt	attattgcgc	gcgtgatttt	300
cttggttatg	agtttgatta	ttggggccaa	ggcacccctgg	tgacggtag	ctcagc	356

<210> 78

<211> 380

<212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VH domain

<400> 78

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cctggcagg	gtctcgagt	gatgggctgg	attaaccga	atagcggcgg	cacgaactac	180
gcccagaagt	ttcagggccg	ggtgaccatg	accctgtata	ccagcattag	caccgcgtat	240
atggaactga	gcagcctg	tagcgaagat	acggccgtgt	attattgcgc	gcgttattat	300
ggttcttctc	tttatcatta	tgttttgg	gtttttattg	attattgggg	ccaaggcacc	360
ctgggtacgg	ttagctcagc					380

<210> 79

<211> 380

<212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VH domain

<400> 79

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agctgcaaag	cctccggata	taccttacc	agctattata	tgcactgggt	ccgccaagcc	120
cctggcagg	gtctcgagt	gatgggctgg	attaaccga	atagcggcgg	cacgaactac	180
gcccagaagt	ttcagggccg	ggtgaccatg	accctgtata	ccagcattag	caccgcgtat	240

atggaactga gcagcctgcg tagcgaagat acggccgtgt attattgcgc gcgtggttat	300
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ctggtgacgg ttagctcagc	380
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<211> 383	
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<400> 80	
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cagtattctt attttatta tcttgatggt gtttattatt ttgatatttg gggccaaggc	360
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<210> 81	
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<212> DNA	
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<220>	
<221> misc_feature	
<222> (1)..(3)	
<223> NNN=GAA OR CAG	
<400> 81	
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cagccgcctg ggaaagccct cgagtggctg gctctgattt attggatga tgataagtat	180
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<210> 82	
<211> 392	
<212> DNA	
<213> Artificial Sequence	
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<223> polynucleotide sequence of a VH domain	
<400> 82	
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acctgtacctt ttccggatt tagcctgtcc acgtctggcg ttggcgtggg ctggattcgc	120
cagccgcctg ggaaagccct cgagtggctg gctctgattt attggatga tgataagtat	180
tatagcacca gcctgaaaac gcgtctgacc attagcaaag atacttcgaa aaatcaggtg	240
gtgctgacta tgaccaacat ggaccggctg gatacggcca cctattatttgcgcgtat	300
cattcttggta atgagatggg ttattatggta tctactgttg gttatatgtt tgattattgg	360

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392

<210> 83
<211> 341
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VH domain

<220>
<221> misc_feature
<222> (1)..(3)
<223> NNN=GAA OR CAG

<400> 83
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cagtctcctg ggcgtggcct cgagtggctg ggccgtacct attatcgttag caaatggtat 180
aacgattatg cggtagcgt gaaaagccgg attaccatca accccgataac ttcgaaaaac 240
cagtttagcc tgcaactgaa cagcgtgacc ccggaagata cggccgtgta ttattgcgcg 300
cgtgattggg gccaaggcac cctggtaac gttagctcag c 341

<210> 84
<211> 362
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VH domain

<400> 84
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acctgtgcga ttccggaga tagcgtgagc agcaacagcg cggcgtggaa ctggattcgc 120
cagtctcctg ggcgtggcct cgagtggctg ggccgtacct attatcgttag caaatggtat 180
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cagtttagcc tgcaactgaa cagcgtgacc ccggaagata cggccgtgta ttattgcgcg 300
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gc 362

<210> 85
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VL domain

<400> 85

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1						5			10				15		

Thr	Ala	Arg	Ile	Ser	Cys	Ser	Gly	Asp	Ala	Leu	Gly	Asp	Lys	Tyr	Ala
20								25				30			

Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr

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35	40	45
Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser		
50	55	60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu		
65	70	75
80		
Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Tyr Ser Ala Asp Tyr		
85	90	95
Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln		
100	105	

<210> 86
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VL domain
<400> 86

Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
20 25 30

Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser His His Phe Tyr
85 90 95

Glu Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
100 105 110

<210> 87
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VL domain
<400> 87

Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1 5 10 15

Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Asp Lys Tyr Ala

20

25

30

Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
 35 40 45

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
 50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
 65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Phe Asp Phe Ala Val
 85 90 95

Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
 100 105

<210> 88

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide sequence of a VL domain

<400> 88

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Arg Ser Ser Gln Ser Val Leu Tyr Ser
 20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
 85 90 95

Tyr Asp Ser Ile Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 100 105 110

Lys Arg Thr
 115

<210> 89

<211> 110

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide sequence of a VL domain

<400> 89

Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly
1					5					10					15
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Ser
				20					25						30
Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu
					35			40							45
Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Val	Pro	Ala	Arg	Phe	Ser
				50				55							60
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Glu
					65			70			75				80
Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Met	Ser	Asn	Tyr	Pro
					85				90						95
Asp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr		
					100				105						110

<210> 90

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide sequence of a VL domain

<400> 90

Asp	Ile	Ala	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser	Pro	Gly	Gln
1						5				10					15
Ser	Ile	Thr	Ile	Ser	Cys	Thr	Gly	Thr	Ser	Ser	Asp	Val	Gly	Gly	Tyr
				20				25							30
Asn	Tyr	Val	Ser	Trp	Tyr	Gln	Gln	His	Pro	Gly	Lys	Ala	Pro	Lys	Leu
				35				40							45
Met	Ile	Tyr	Asp	Val	Ser	Asn	Arg	Pro	Ser	Gly	Val	Ser	Asn	Arg	Phe
				50				55			60				
Ser	Gly	Ser	Lys	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Ser	Gly	Leu
					65			70			75				80
Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Ser	Tyr	Asp	Asn	Asn
					85				90						95
Ser	Asp	Val	Val	Phe	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	Gln	
				100					105						110

<210> 91

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide sequence of a VL domain

<400> 91

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5					10					15	

Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Gly	Ile	Ser	Ser	Tyr
	20				25							30			

Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
	35				40							45			

Tyr	Ala	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50				55						60				

Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65				70				75					80		

Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Phe	Gln	Tyr	Gly	Ser	Ile	Pro	Pro
				85				90					95		

Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr			
					100		105								

<210> 92

<211> 110

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide sequence of a VL domain

<400> 92

Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly
1				5					10					15	

Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Ser
	20				25							30			

Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu
	35				40							45			

Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Val	Pro	Ala	Arg	Phe	Ser
	50				55							60			

Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Glu
65					70				75					80	

Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Thr	Asn	Asn	Ala	Pro
					85				90					95	

Val	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr		
						100		105				110			

<210> 93

<211> 108

<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VL domain

<400> 93

Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1 5 10 15

Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Asp Lys Tyr Ala
20 25 30

Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Tyr Phe Lys Leu Val
85 90 95

Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
100 105

<210> 94
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VL domain

<400> 94

Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
20 25 30

Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Met Tyr
85 90 95

Asn Tyr Ile Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
100 105 110

<210> 95
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VL domain
<400> 95

Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1 5 10 15

Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Asp Lys Tyr Ala
20 25 30

Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Gly Pro Asp Leu Trp
85 90 95

Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
100 105

<210> 96
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VH domain
<400> 96

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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Ala Arg Asp Phe Leu Gly Tyr Glu Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 97
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VH domain

<400> 97

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Gly Ser Ser Leu Tyr His Tyr Val Phe Gly Gly Phe
100 105 110

Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 98
<211> 130
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VH domain

<400> 98

Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
 50 55 60

Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
 85 90 95

Cys Ala Arg Tyr His Ser Trp Tyr Glu Met Gly Tyr Tyr Gly Ser Thr
 100 105 110

Val Gly Tyr Met Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
 115 120 125

Ser Ser
 130

<210> 99
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> polypeptide sequence of a VH domain
 <400> 99

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
 20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Asn Trp Phe Lys Pro Phe Ser Asp Val Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 100
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> polypeptide sequence of a VH domain

<400> 100

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser
1					5				10				15		

Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Phe	Ser	Ser	Tyr
					20			25				30			

Ala	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
					35			40				45			

Gly	Gly	Ile	Ile	Pro	Ile	Phe	Gly	Thr	Ala	Asn	Tyr	Ala	Gln	Lys	Phe
					50			55			60				

Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Glu	Ser	Thr	Ser	Thr	Ala	Tyr
					65			70		75				80	

Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
					85			90			95				

Ala	Arg	Val	Asn	His	Trp	Thr	Tyr	Thr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly
					100			105			110				

Thr	Leu	Val	Thr	Val	Ser	Ser									
					115										

<210> 101

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide sequence of a VH domain

<400> 101

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala
1					5				10				15		

Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr
					20			25			30				

Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
					35			40				45			

Gly	Trp	Ile	Asn	Pro	Asn	Ser	Gly	Gly	Thr	Asn	Tyr	Ala	Gln	Lys	Phe
					50			55			60				

Gln	Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	Ser	Ile	Ser	Thr	Ala	Tyr
					65			70		75				80	

Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
					85			90			95				

Ala	Arg	Gly	Tyr	Trp	Tyr	Ala	Tyr	Phe	Thr	Tyr	Ile	Asn	Tyr	Gly	Tyr
					100			105			110				

Phe	Asp	Asn	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser		
					115			120			125				

<210> 102
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VH domain
<400> 102

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Trp Val Ser His Gly Tyr Tyr Tyr Leu Phe Asp
100 105 110

Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 103
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VH domain
<400> 103

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Thr Trp Gln Tyr Ser Tyr Phe Tyr Tyr Leu Asp Gly Gly Tyr
 100 105 110

Tyr Phe Asp Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 104

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide sequence of a VH domain

<400> 104

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asn Met Ala Tyr Thr Asn Tyr Gln Tyr Val Asn Met Pro His
 100 105 110

Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 105

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide sequence of a VH domain

<400> 105

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Ser Met Asn Ser Thr Met Tyr Trp Tyr Leu Arg Arg Val Leu
 100 105 110

Phe Asp His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 106
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VH domain

<400> 106

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
 20 25 30

Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu
 35 40 45

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
 50 55 60

Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
 65 70 75 80

Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
 85 90 95

Tyr Tyr Cys Ala Arg Ser Tyr Tyr Pro Asp Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120